

A

| Oilgo # | Name | Primer Sequences (5'-3') |
|---------|------|--------------------------|
| 2663 | mK1 | TTG GTG CTG ATG TTC TGG |
| 2664 | mK2 | ATC TTC TTG CTG TTC TGG |
| 2665 | mK3 | TGG GTG CTG CTG CTC TGG |
| 2666 | mK4 | GGG CTG CTT GTG CTC TGG |
| 2667 | mK5 | GGA ATC TTG TTG CTC TGG |
| 2668 | mK6 | RTR TTS CTG CTG CTR TGG |
| 2669 | mK7 | GGT CTC CTG TTG CTC TGT |
| 2670 | mK8 | ATA TTT CTA CTG CTC TGT |
| 2671 | mK9 | GTC ATA ATR TCC AGA GGA |

B

| Oilgo # | Name | Primer Sequences (5'-3') |
|---------|------|--------------------------|
| 2672 | mH1 | CTG AGC TGT GTA TTC CT |
| 2673 | mH2 | CTC ARM TTG ATT TTC CT |
| 2674 | mH3 | TGG RTC ATS TTC TTC CT |
| 2675 | mH4 | TKS RTC TTT CTC TTC CT |
| 2676 | mH5 | TGT ATC ATS CTC TTC TT |
| 2677 | mH6 | TGG RTC TTT CTC TTT TT |
| 2678 | mH7 | TTA AAC TGG GTT TTT CT |
| 2679 | mH8 | GKG CTG YTC YTC TGC CT |
| 2680 | mH9 | TTA AGT CTT CTG TAC CTG |
| 2730 | MH11 | TCAGTAACTGCAGGTGTCCA |
| 2731 | MH12 | TTTTAAAAGGTGTCCAGTGT |
| 2732 | MH13 | GCAACAGCTACAGGTGTCCA |
| 2733 | MH14 | CAGCTACAGRTGTCCACTCC |
| 2734 | MH15 | ATTCCAAGCTGTGTCCTGTCC |
| 2735 | MH16 | CTCCTGTCAGGAACTGCAGGTGT |
| 2736 | MH17 | CAGTGGTTACAGGGGTCAATTCA |
| 2737 | MH18 | CTGTTSACAGCCHTTCKGGT |
| 2738 | MH19 | CTGATGGCAGCTGCCCAAAGT |
| 2739 | MH20 | TTTATCAAGGTGTGCATTGT |

C

2650 5' TCACTGGATGGTGGGAAGATGGATACA 3'
2656 5' GACATTTGGGAAGGACTGACTCTC 3'
2706 5' CAG GGG GCT CTC GCA GGA GAC GAG 3'

FIGURE 1

Attorney Docket: P-IX 4976
Inventors: Watkins et al.

HuIV-26 VL

GACATTGTGATGACACAGTCTCCATCTTTGTTGAGTGTGTCAGCAGGAGAGAAGGTCACT
ATGAGCTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTACTTGGCC
TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGTTGATCTATGGGGCATCCACTAGG
GAATCTGGGGTCCCTGATCGCTTACAGGCAGTGGATCTGGAACCGATTTCCTCTTATC
ATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGAATGATCATAGTTAT
CCGTACACGTTTCGGAGGGGGGACCAAGCTGGAAATAAAA

FIGURE 2A

HuIV-26 VH

GAGGTGAAGCTTCTCGAGTCTGGAGGTGGCCTGGTGCAGCCTGGAGGATCCCTGAAACT
CTCCTGTGCAGCCTCAGGATTGATTTTAGTAGATACTGGATGAGTTGGGTCCGGCAGG
CTCCAGGGAAAGGGCTAGAATGGATTGGAGAAATTAATCCAGATAGCAGTACGATAAAC
TATACGCCATCTCTAAAGGATAAATTCATCATCTCCAGAGACAACGCCAAAAATACGCT
GTACCTGCAAATGAGCAAAGTGAGATCTGAGGACACAGCCCTTTATTACTGTGCAAGAC
CGGTTGATGGTTACTACGATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTC
TCCTCA

FIGURE 2B

FIG. 2C

Vk Domain

| | | | | | |
|----------|----|-------|-------|--------|----------------|
| | 1 | 10 | 20 | 30 | 40 |
| HUIV26 | DI | VTQSP | LLSV | AGEKVT | MSCKSSQSL |
| | | | | | NSGNQKNYLA |
| | | | | | WYQQKPGQPKLLIY |
| VKIV | DI | VTQSP | DSLA | VS | LG |
| | | | | | ERATINCKSSQSV |
| | | | | | LYSSNNKNYLA |
| | | | | | WYQQKPGQPKLLIY |
| | 50 | 60 | 70 | 80 | 90 |
| HUIV26 | GA | STR | ESGVP | DRFT | GTGSG |
| | | | | | TDFTLI |
| | | | | | ISSVQAEDLA |
| | | | | | VYQCNDH |
| | | | | | SYPTFGG |
| | | | | | G |
| | | | | | TKLEIK |
| VKIV/JK2 | WA | STR | ESGVP | DRFT | GTGSG |
| | | | | | TDFTLT |
| | | | | | ISSLQAEDVA |
| | | | | | VYCCQDDH |
| | | | | | SYPTFGG |
| | | | | | G |
| | | | | | TKLEIK |

VH Domain

| | | | | | |
|--------|-----|-----|-------|-----|-----------|
| | 1 | 10 | 20 | 30 | 40 |
| HUIV26 | EV | KLL | ESGG | LVQ | PGGSL |
| | | | | | KLSCAAS |
| | | | | | GFDFSR |
| | | | | | YWM |
| | | | | | SVRQAPG |
| | | | | | KGLEWIG |
| VHIII | EV | QL | VESGG | LVQ | PGGSL |
| | | | | | RLRLSCAAS |
| | | | | | GFDFSS |
| | | | | | YWM |
| | | | | | SVRQAPG |
| | | | | | KGLEWVA |
| | 50 | 60 | 70 | 80 | 90 |
| HUIV26 | EI | NP | DSST | IN | YT |
| | | | | | TPSLK |
| | | | | | DKFII |
| | | | | | ISR |
| | | | | | DN |
| | | | | | AKNTLY |
| | | | | | LQMSK |
| | | | | | VRSEDTA |
| | | | | | LYYCAR |
| VHIII | NI | KQ | DGSE | KYY | V |
| | | | | | DSV |
| | | | | | KGRFT |
| | | | | | ISR |
| | | | | | DN |
| | | | | | AKNSLY |
| | | | | | LQMNS |
| | | | | | LR |
| | | | | | AE |
| | | | | | DTA |
| | | | | | VY |
| | | | | | YCAR |
| | abc | 100 | 110 | | |
| HUIV26 | P | V | D | G | Y |
| | | | | | D |
| | | | | | A |
| | | | | | M |
| | | | | | D |
| | | | | | Y |
| | | | | | W |
| | | | | | G |
| | | | | | Q |
| | | | | | T |
| | | | | | S |
| JH6 | P | D | Y | Y | Y |
| | | | | | G |
| | | | | | M |
| | | | | | D |
| | | | | | V |
| | | | | | W |
| | | | | | G |
| | | | | | Q |
| | | | | | T |
| | | | | | T |
| | | | | | V |
| | | | | | S |

FIGURE 2C

HUI77 VL sequence

GATGTTTTGATGACCCAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCC
ATCTCTTGCAGATCTAGTCAGAGCATTGTACATAGTAATGGAAACACCTATTTAGAATGG
TACCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCGATTT
TCTGGTGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCAAGATC
AGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTACTGCTTCAAGGTTACATGTTCCG
TGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA

FIGURE 3A

HUI77 VH SEQUENCE

CAGGTTACTCTGAAAGAGACTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTCAGTCTG
ACTTGTTCTTTCTCTGGGTTTTCACTGAGCACTTCTGGTATGGGTGTAGGCTGGATTCGT
CAGCCTTCAGGAGAGGGTCTAGAGTGGCTGGCAGACATTTGGTGGGATGACAATAAGTAC
TATAACCCATCCCTGAAGAGCCGGCTCACAATCTCCAAGGATACCTCCAGCAACCAGGTA
TTCCTCAAGATCACCAGTGTGGACACTGCAGATACTGCCACTTACTACTGTGCTCGAAGA
GCTAACTATGGTAACCCCTACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACC
GTCTCCTCA

FIGURE 3B

Vk Domain

| | | | | | |
|----------|----|----|----|----|----|
| | 1 | 10 | 20 | 30 | 40 |
| HUI-77 | D | V | L | M | T |
| VKII | D | I | V | M | T |
| | 50 | 60 | 70 | 80 | 90 |
| HUI-77 | K | V | S | N | R |
| VKII/JK1 | T | L | S | R | A |

VH Domain

| | | | | | |
|--------|-----|-----|----|----|----|
| | 1 | 10 | 20 | 30 | 40 |
| HUI-77 | Q | V | T | L | K |
| VHII | Q | V | T | L | K |
| | 50 | 60 | 70 | 80 | 90 |
| HUI-77 | D | I | W | D | D |
| VHII | R | I | D | W | D |
| | 100 | 110 | | | |
| HUI-77 | R | A | N | Y | G |
| JH6 | R | A | N | Y | G |

FIGURE 3C

HUI77 VL sequence

| | | | | | | | | | | | | | | | |
|----------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 |
| HUI77 VL | GAT | GTT | TTG | ATG | ACC | CAA | ACT | CCA | CTC | TCC | CTG | CCT | GTC | AGT | CTT |
| DPK13 | --- | A-- | G-- | --- | --- | --G | --- | --- | --- | --- | --- | --C | --- | -CC | -C- |
| | CDR1 | | | | | | | | | | | | | | |
| | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 27a | 27b | 27c |
| HUI77 VL | GGA | GAT | CAA | GCC | TCC | ATC | TCT | TGC | AGA | TCT | AGT | CAG | AGC | ATT | GTA |
| DPK13 | --- | --G | -CG | --- | --- | --- | --C | --- | --G | --- | --- | --- | --- | C-C | T-G |
| | 27d | 27e | 27f | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 |
| HUI77 VL | CAT | AGT | ... | AAT | GGA | AAC | ACC | TAT | TTA | GAA | TGG | TAC | CTG | CAG | AAA |
| DPK13 | G-- | --- | GAT | G-- | --- | --- | --- | --- | --G | --C | --- | --- | --- | --- | --G |
| | CDR2 | | | | | | | | | | | | | | |
| | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 |
| HUI77 VL | CCA | GGC | CAG | TCT | CCA | AAG | CTC | CTG | ATC | TAC | AAA | GTT | TCC | AAC | CGA |
| DPK13 | --- | --G | --- | --- | --- | C-- | --- | --- | --- | --T | -CG | C-- | --- | T-T | --G |
| | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 |
| HUI77 VL | TTT | TCT | GGT | GTC | CCA | GAC | AGG | TTC | AGT | GGC | AGT | GGA | TCA | GGG | ACA |
| DPK13 | GCC | --- | --A | --- | --- | --- | --- | --- | --- | --- | --- | --G | --- | --C | --T |
| | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 |
| HUI77 VL | GAT | TTC | ACA | CTC | AAG | ATC | AGC | AGA | GTG | GAG | GCT | GAG | GAT | CTG | GGA |
| DPK13 | --- | --- | --- | --G | --A | --- | --- | --G | --- | --- | --- | --- | --- | G-T | --- |
| | CDR3 | | | | | | | | | | | | | | |
| | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 |
| HUI77 VL | GTT | TAT | TAC | TGC | TTT | CAA | GGT | TCA | CAT | GTT | CCG | TGG | ACG | TTC | GGT |
| DPK13 | --- | --- | --- | --- | A-G | --- | --- | --- | --- | --- | --- | --- | --- | --- | --C |
| | 100 | 101 | 102 | 103 | 104 | 105 | 106 | 107 | | | | | | | |
| HUI77 VL | GGA | GGC | ACC | AAG | CTG | GAA | ATC | AAA | | | | | | | |
| JK1 | CA- | --G | --- | --- | G-- | --- | --- | --- | | | | | | | |

FIGURE 3D

HUIV26 LCDR3

IV26-17.1 CTT GGT CCC CTG GCC AAA AGT GTA CGG ATA ACT ATG ATC ATT MNN ACA GTA ATA AAC TGC CAC ATC
IV26-17.2 CTT GGT CCC CTG GCC AAA AGT GTA CGG ATA ACT ATG ATC MNN CTG ACA GTA ATA AAC TGC CAC ATC
IV26-17.3 CTT GGT CCC CTG GCC AAA AGT GTA CGG ATA ACT ATG MNN ATT CTG ACA GTA ATA AAC TGC CAC ATC
IV26-17.4 CTT GGT CCC CTG GCC AAA AGT GTA CGG ATA ACT MNN ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC
IV26-17.5 CTT GGT CCC CTG GCC AAA AGT GTA CGG ATA MNN ATG ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC
IV26-17.6 CTT GGT CCC CTG GCC AAA AGT GTA CGG MNN ACT ATG ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC
IV26-17.7 CTT GGT CCC CTG GCC AAA AGT GTA MNN ATA ACT ATG ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC
IV26-17.8 CTT GGT CCC CTG GCC AAA AGT MNN CGG ATA ACT ATG ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC
IV26-17.9 CTT GGT CCC CTG GCC AAA MNN GTA CGG ATA ACT ATG ATC ATT CTG ACA GTA ATA AAC TGC CAC ATC

HUIV26 HCDR3

IV26-h7.1 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC GTA GTA ACC ATC AAC MNN TCT CGC ACA GTA ATA CAC
IV26-h7.2 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC GTA GTA ACC ATC MNN CGG TCT CGC ACA GTA ATA CAC
IV26-h7.3 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC GTA GTA ACC MNN AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.4 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC GTA GTA MNN ATC AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.5 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC GTA MNN ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.6 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATC MNN GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.7 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC MNN GTA GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.8 CGT GGT TCC TTG CCC CCA GTA GTC CAT MNN ATC GTA GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.9 CGT GGT TCC TTG CCC CCA GTA GTC MNN AGC ATC GTA GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.10 CGT GGT TCC TTG CCC CCA GTA MNN CAT AGC ATC GTA GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC
IV26-h7.11 CGT GGT TCC TTG CCC CCA MNN GTC CAT AGC ATC GTA GTA ACC ATC AAC CGG TCT CGC ACA GTA ATA CAC

FIGURE 4A

Attorney Docket: P-IX 4976
Inventors: Watkins et al.

HUIV26 LCDR1a

IV26L1-1 GTTCTTTTGGTTTCCGCWGTTTAACAGACTCTGGCTGGAMNNGCAGTTGATGGTGGCCCT
IV26L1-2 GTTCTTTTGGTTTCCGCWGTTTAACAGACTCTGGCTMNNTTGCAGTTGATGGTGGCCCT
IV26L1-3 GTTCTTTTGGTTTCCGCWGTTTAACAGACTCTGMNNGGACTTGCAGTTGATGGTGGCCCT
IV26L1-4 GTTCTTTTGGTTTCCGCWGTTTAACAGACTMNNGCTGGACTTGCAGTTGATGGTGGCCCT
IV26L1-5 GTTCTTTTGGTTTCCGCWGTTTAACAGMNNCTGGCTGGACTTGCAGTTGATGGTGGCCCT
IV26L1-6 GTTCTTTTGGTTTCCGCWGTTTAAMNNACTCTGGCTGGACTTGCAGTTGATGGTGGCCCT
IV26L1-7 GTTCTTTTGGTTTCCGCWGTTMNNAAGACTCTGGCTGGACTTGCAGTTGATGGTGGCCCT
IV26L1-8 GTTCTTTTGGTTTCCGCWMNNTAACAGACTCTGGCTGGACTTGCAGTTGATGGTGGCCCT

HUIV26 LCDR1b

IV26L1-9 TGGTTTCTGCTGGTACCAAGCTAAGTAGTTCTTTTGGTTTCCMNNGTTTAAACAGACTCTGGCT
IV26L1-10 TGGTTTCTGCTGGTACCAAGCTAAGTAGTTCTTTTGGTTMNNGCWGTTTAACAGACTCTGGCT
IV26L1-11 TGGTTTCTGCTGGTACCAAGCTAAGTAGTTCTTTTGMNNTCCGCWGTTTAACAGACTCTGGCT
IV26L1-12 TGGTTTCTGCTGGTACCAAGCTAAGTAGTTCTTMNNGTTTCCGCWGTTTAACAGACTCTGGCT
IV26L1-13 TGGTTTCTGCTGGTACCAAGCTAAGTAGTTMNNTTGGTTTCCGCWGTTTAACAGACTCTGGCT
IV26L1-14 TGGTTTCTGCTGGTACCAAGCTAAGTAMNNCTTTTGGTTTCCGCWGTTTAACAGACTCTGGCT
IV26L1-15 TGGTTTCTGCTGGTACCAAGCTAAMNNGTTCTTTTGGTTTCCGCWGTTTAACAGACTCTGGCT
IV26L1-16 TGGTTTCTGCTGGTACCAAGCMNNGTAGTTCTTTTGGTTTCCGCWGTTTAACAGACTCTGGCT
IV26L1-17 TGGTTTCTGCTGGTACCAMNNTAAGTAGTTCTTTTGGTTTCCGCWGTTTAACAGACTCTGGCT

HUIV26 LCDR2

IV26L2-1 GAATCGGTCAAGGACCCCGGATTCCCTGGTAGATGCMNNGTAAATGAGCAGCTTAGG
IV26L2-2 GAATCGGTCAAGGACCCCGGATTCCCTGGTAGAMNCCCGTAAATGAGCAGCTTAGG
IV26L2-3 GAATCGGTCAAGGACCCCGGATTCCCTGGTMNNTGCCCGTAAATGAGCAGCTTAGG
IV26L2-4 GAATCGGTCAAGGACCCCGGATTCCCTMNNAGATGCCCGTAAATGAGCAGCTTAGG
IV26L2-5 GAATCGGTCAAGGACCCCGGATTMNNNGTAGATGCCCGTAAATGAGCAGCTTAGG
IV26L2-6 GAATCGGTCAAGGACCCCGGAMNNTCTGGTAGATGCCCGTAAATGAGCAGCTTAGG
IV26L2-7 GAATCGGTCAAGGACCCCMNNTTCCCTGGTAGATGCCCGTAAATGAGCAGCTTAGG

HUIV26 HCDR1

IV26H1-1 TGGAGCCTGGCGGACCCAGCTCATCCAATAMNNACTAAAGGTGAATCCAGA
IV26H1-2 TGGAGCCTGGCGGACCCAGCTCATCCAMNNTCTACTAAAGGTGAATCCAGA
IV26H1-3 TGGAGCCTGGCGGACCCAGCTCATMNNATATCTACTAAAGGTGAATCCAGA
IV26H1-4 TGGAGCCTGGCGGACCCAGCTMNNCAATATCTACTAAAGGTGAATCCAGA
IV26H1-5 TGGAGCCTGGCGGACCCAMNNCATCCAATATCTACTAAAGGTGAATCCAGA

HUIV26 HCDR2a

IV26H2-1 TAGAGATGGCGTATAGTTTATCGTACTGCTATCTGGATTATMNNGCCAAYCCACTCCAGCCCTTTC
IV26H2-2 TAGAGATGGCGTATAGTTTATCGTACTGCTATCTGGATTMNNNTCGCCAAYCCACTCCAGCCCTTTC
IV26H2-3 TAGAGATGGCGTATAGTTTATCGTACTGCTATCTGGMNNTATTTGCCAAYCCACTCCAGCCCTTTC
IV26H2-4 TAGAGATGGCGTATAGTTTATCGTACTGCTATCMNNATTATTTGCCAAYCCACTCCAGCCCTTTC
IV26H2-5 TAGAGATGGCGTATAGTTTATCGTACTGCTMNNNTGGATTATTTGCCAAYCCACTCCAGCCCTTTC
IV26H2-6 TAGAGATGGCGTATAGTTTATCGTACTMNNATCTGGATTATTTGCCAAYCCACTCCAGCCCTTTC
IV26H2-7 TAGAGATGGCGTATAGTTTATCGTMNNGCTATCTGGATTATTTGCCAAYCCACTCCAGCCCTTTC
IV26H2-8 TAGAGATGGCGTATAGTTTATMNNACTGCTATCTGGATTATTTGCCAAYCCACTCCAGCCCTTTC
IV26H2-9 TAGAGATGGCGTATAGTTMNNCGTACTGCTATCTGGATTATTTGCCAAYCCACTCCAGCCCTTTC

HUIV26 HCDR2b

IV26H2-10 CGTTGTCTCTGGAGATGRTGAATYATCCTTTAGAGATGGCGTATAMNNNTATCGTACTGCTATCTGG
IV26H2-11 CGTTGTCTCTGGAGATGRTGAATYATCCTTTAGAGATGGCGTMNNGTTTATCGTACTGCTATCTGG
IV26H2-12 CGTTGTCTCTGGAGATGRTGAATYATCCTTTAGAGATGGMNNATAGTTTATCGTACTGCTATCTGG
IV26H2-13 CGTTGTCTCTGGAGATGRTGAATYATCCTTTAGAGAMNNGTATAGTTTATCGTACTGCTATCTGG
IV26H2-14 CGTTGTCTCTGGAGATGRTGAATYATCCTTTAGMNNNTGGCGTATAGTTTATCGTACTGCTATCTGG
IV26H2-15 CGTTGTCTCTGGAGATGRTGAATYATCCTTMNNAGATGGCGTATAGTTTATCGTACTGCTATCTGG
IV26H2-16 CGTTGTCTCTGGAGATGRTGAATYATCMNNNTAGAGATGGCGTATAGTTTATCGTACTGCTATCTGG
IV26H2-17 CGTTGTCTCTGGAGATGRTGAATYTMNNCTTTAGAGATGGCGTATAGTTTATCGTACTGCTATCTGG

FIGURE 4B

Beneficial Mutations for HuIV-26 Antibody

| CDRs | H1 | | | H2 | | | | H3 | | | L1 | | | | | L2 | L3 | |
|--------------|----|----|----|----|----|----|----|----|----|-----|----|-----|-----|-----|----|----|----|----|
| Kabat Number | 31 | 34 | 35 | 57 | 62 | 64 | 65 | 97 | 98 | 102 | 27 | 27d | 27e | 27f | 29 | | 93 | 94 |
| HuIV-26 | R | M | S | I | S | K | D | D | G | Y | Q | N | S | G | Q | | S | Y |
| Mutations | H | I | T | A | Y | Q | S | P | P | P | R | S | Y | Y | K | | Q | N |
| | | | A | S | A | | | G | A | N | S | | W | R | | | G | S |
| | | | G | | H | | | T | H | | | | H | H | | | L | P |
| | | | | | G | | | A | | | | | R | I | | | A | M |
| | | | | | | | | | | | | | | | | | T | |
| | | | | | | | | | | | | | | | | | V | |

FIGURE 4C

Attorney Docket: P-IX 4976
Inventors: Watkins et al.

HUI77 LCDR3

I77-I7.1 CTT GGT GCC CTG GCC GAA CGT CCA CGG AAC ATG TGA ACC TTG MNN GCA GTA ATA AAC TCC AAC ATC
I77-I7.2 CTT GGT GCC CTG GCC GAA CGT CCA CGG AAC ATG TGA ACC MNN AAA GCA GTA ATA AAC TCC AAC ATC
I77-I7.3 CTT GGT GCC CTG GCC GAA CGT CCA CGG AAC ATG TGA MNN TTG AAA GCA GTA ATA AAC TCC AAC ATC
I77-I7.4 CTT GGT GCC CTG GCC GAA CGT CCA CGG AAC ATG MNN ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC
I77-I7.5 CTT GGT GCC CTG GCC GAA CGT CCA CGG AAC MNN TGA ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC
I77-I7.6 CTT GGT GCC CTG GCC GAA CGT CCA CGG MNN ATG TGA ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC
I77-I7.7 CTT GGT GCC CTG GCC GAA CGT CCA MNN AAC ATG TGA ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC
I77-I7.8 CTT GGT GCC CTG GCC GAA CGT MNN CGG AAC ATG TGA ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC
I77-I7.9 CTT GGT GCC CTG GCC GAA MNN CCA CGG AAC ATG TGA ACC TTG AAA GCA GTA ATA AAC TCC AAC ATC

HUI77 HCDR3

I77-h7.1 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG GTT ACC ATA GTT AGC MNN TCG AGC ACA GTA ATA CGT
I77-h7.2 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG GTT ACC ATA GTT MNN TCT TCG AGC ACA GTA ATA CGT
I77-h7.3 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG GTT ACC ATA MNN AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.4 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG GTT ACC MNN GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.5 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG GTT MNN ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.6 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA GGG MNN ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.7 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA GTA MNN GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.8 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC ATA MNN GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.9 CGT GGT TCC TTG CCC CCA GTA GTC CAT AGC MNN GTA GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.10 CGT GGT TCC TTG CCC CCA GTA GTC CAT MNN ATA GTA GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.11 CGT GGT TCC TTG CCC CCA GTA GTC MNN AGC ATA GTA GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.12 CGT GGT TCC TTG CCC CCA GTA MNN CAT AGC ATA GTA GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT
I77-h7.13 CGT GGT TCC TTG CCC CCA MNN GTC CAT AGC ATA GTA GGG GTT ACC ATA GTT AGC TCT TCG AGC ACA GTA ATA CGT

FIGURE 5A

HUI77 LCDR1a

3000 ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT AGA MNN GCA GGA GAT GGA GGC C
3001 ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT MNN CCT GCA GGA GAT GGA GGC C
3002 ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG MNN AGA CCT GCA GGA GAT GGA GGC C
3003 ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT MNN ACT AGA CCT GCA GGA GAT GGA GGC C
3004 ATA GGT GTT TCC ATT ACT ATG TAC AAT MNN CTG ACT AGA CCT GCA GGA GAT GGA GGC C
3005 ATA GGT GTT TCC ATT ACT ATG TAC MNN GCT CTG ACT AGA CCT GCA GGA GAT GGA GGC C
3006 ATA GGT GTT TCC ATT ACT ATG MNN AAT GCT CTG ACT AGA CCT GCA GGA GAT GGA GGC C
3007 ATA GGT GTT TCC ATT ACT MNN TAC AAT GCT CTG ACT AGA CCT GCA GGA GAT GGA GGC C

HUI77 LCDR1b

3008 TGG CTT CTG CAG GTA CCA TTC CAA ATA GGT GTT TCC ATT MNN ATG TAC AAT GCT CTG ACT
3009 TGG CTT CTG CAG GTA CCA TTC CAA ATA GGT GTT TCC MNN ACT ATG TAC AAT GCT CTG ACT
3010 TGG CTT CTG CAG GTA CCA TTC CAA ATA GGT GTT MNN ATT ACT ATG TAC AAT GCT CTG ACT
3011 TGG CTT CTG CAG GTA CCA TTC CAA ATA GGT MNN TCC ATT ACT ATG TAC AAT GCT CTG ACT
3012 TGG CTT CTG CAG GTA CCA TTC CAA ATA MNN GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT
3013 TGG CTT CTG CAG GTA CCA TTC CAA MNN GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT
3014 TGG CTT CTG CAG GTA CCA TTC MNN ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT
3015 TGG CTT CTG CAG GTA CCA MNN CAA ATA GGT GTT TCC ATT ACT ATG TAC AAT GCT CTG ACT

HUI77 LCDR2

3016 GAA CCT GTC TGG GAC TCC AGA AAA CCG GTT GGA AAC MNN ATA GAT CAG GAG CTG TGG
3017 GAA CCT GTC TGG GAC TCC AGA AAA CCG GTT GGA MNN TTT ATA GAT CAG GAG CTG TGG
3018 GAA CCT GTC TGG GAC TCC AGA AAA CCG GTT MNN AAC TTT ATA GAT CAG GAG CTG TGG
3019 GAA CCT GTC TGG GAC TCC AGA AAA CCG MNN GGA AAC TTT ATA GAT CAG GAG CTG TGG
3020 GAA CCT GTC TGG GAC TCC AGA AAA MNN GTT GGA AAC TTT ATA GAT CAG GAG CTG TGG
3021 GAA CCT GTC TGG GAC TCC AGA MNN CCG GTT GGA AAC TTT ATA GAT CAG GAG CTG TGG
3022 GAA CCT GTC TGG GAC TCC MNN AAA CCG GTT GGA AAC TTT ATA GAT CAG GAG CTG TGG

HUI77 HCDR1

3023 TGG GGG CTG ACG GAT CCA GCC CAC ACC CAT TCC AGA MNN GCT GAG TGA GAA CCC AGA
3024 TGG GGG CTG ACG GAT CCA GCC CAC ACC CAT TCC MNN AGT GCT GAG TGA GAA CCC AGA
3025 TGG GGG CTG ACG GAT CCA GCC CAC ACC CAT MNN AGA AGT GCT GAG TGA GAA CCC AGA
3026 TGG GGG CTG ACG GAT CCA GCC CAC ACC MNN TCC AGA AGT GCT GAG TGA GAA CCC AGA
3027 TGG GGG CTG ACG GAT CCA GCC CAC MNN CAT TCC AGA AGT GCT GAG TGA GAA CCC AGA
3028 TGG GGG CTG ACG GAT CCA GCC MNN ACC CAT TCC AGA AGT GCT GAG TGA GAA CCC AGA
3029 TGG GGG CTG ACG GAT CCA MNN CAC ACC CAT TCC AGA AGT GCT GAG TGA GAA CCC AGA

HUI77 HCDR2a

3038 CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA AAT MNN TGC AAG CCA CTC CAG GGC
3039 CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA MNN GTC TGC AAG CCA CTC CAG GGC
3040 CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA MNN AAT GTC TGC AAG CCA CTC CAG GGC
3041 CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC MNN CCA AAT GTC TGC AAG CCA CTC CAG GGC
3042 CAG AGA TGG GTT GTA GTA TTT ATT GTC MNN CCA CCA AAT GTC TGC AAG CCA CTC CAG GGC
3043 CAG AGA TGG GTT GTA GTA TTT ATT MNN ATC CCA CCA AAT GTC TGC AAG CCA CTC CAG GGC
3044 CAG AGA TGG GTT GTA GTA TTT MNN GTC ATC CCA CCA AAT GTC TGC AAG CCA CTC CAG GGC
3045 CAG AGA TGG GTT GTA GTA MNN ATT GTC ATC CCA CCA AAT GTC TGC AAG CCA CTC CAG GGC

HUI77 HCDR2b

3030 CTT GGA GAT GGT GAG CCT GCT CTT CAG AGA TGG GTT GTA MNN TTT ATT GTC ATC CCA CCA
3031 CTT GGA GAT GGT GAG CCT GCT CTT CAG AGA TGG GTT MNN GTA TTT ATT GTC ATC CCA CCA
3032 CTT GGA GAT GGT GAG CCT GCT CTT CAG AGA TGG MNN GTA GTA TTT ATT GTC ATC CCA CCA
3033 CTT GGA GAT GGT GAG CCT GCT CTT CAG AGA MNN GTT GTA GTA TTT ATT GTC ATC CCA CCA
3034 CTT GGA GAT GGT GAG CCT GCT CTT CAG MNN TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA
3035 CTT GGA GAT GGT GAG CCT GCT CTT MNN AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA
3036 CTT GGA GAT GGT GAG CCT GCT MNN CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA
3037 CTT GGA GAT GGT GAG CCT MNN CTT CAG AGA TGG GTT GTA GTA TTT ATT GTC ATC CCA CCA

FIGURE 5B

Beneficial Mutations for Hui-77 Antibody

| CDRs | H1 | H2 | H3 | L1 | L2 | L3 |
|--------------|-----------------|---------------|------------------------------------|------------------------|----------------|----------------------------------|
| Kabat Number | 32 35b | 59 64 | 95 100 100e 102 | 27c 27d 27e 28 30 33 | 50 51 53 54 56 | 89 90 91 92 93 94 97 |
| Hui-77 | S G | Y K | R N M Y | V H S N N L | K V N R S | F Q G S H V T |
| Mutations | P W W L A | S P A P | P V Q K Q W N T M L T H V | P L W Y Y F W S W V | S A S L W F | V R S W L T A H W E T S H K I |

Beneficial mutations chosen for combinatorial library

| CDRs | H1 | H2 | H3 | L1 | L3 | SPEkon | SPEkoff |
|--------------|--------|---------------|-----|--------------------------|----|---------|---------|
| Kabat Number | 35 | 57 62 | 102 | 27d 27e 27f | 93 | O.D.560 | O.D.560 |
| wild type | S | I S | Y | N S G | S | | |
| HuIV-26 | S | I S | Y | N S G | S | | |
| Mutations | T A | A Y A H | P | S Y Y W R H H R | Q | | |

Beneficial mutants

| | | | | | | | |
|----------|---|-----|---|-------|---|-------|-------|
| 4.1-2D4 | S | I S | P | N S G | Q | | |
| L1b-F11 | S | I S | P | N S Y | Q | 0.745 | 0.483 |
| H2a-G8 | S | A S | P | N S G | Q | 0.397 | 0.159 |
| 2D4H1-C3 | A | I S | P | N S G | Q | | |
| DcomA4 | S | A Y | P | N Y Y | Q | 0.981 | 0.769 |
| DcomB1 | A | A Y | P | N Y H | Q | 1.018 | 0.714 |
| DcomE1 | | | | | | 1.031 | 0.758 |
| DcomH2 | | | | | | 1.07 | 0.705 |
| DcomD2 | S | A S | P | N R Y | Q | 1.104 | 0.729 |
| DcomD3 | T | A Y | P | N S Y | Q | 1.035 | 0.736 |
| DcomD6 | S | A Y | P | N W Y | Q | 1.102 | 0.753 |
| DcomA11 | | | | | | 1.003 | 0.786 |
| DcomE3 | T | A Y | P | N R Y | Q | 0.991 | 0.754 |
| DcomG2 | A | A Y | P | N R Y | Q | 1.161 | 0.856 |
| DcomA7 | T | V S | P | N Y Y | Q | 0.986 | 0.77 |
| DcomB8 | T | A A | P | N W Y | Q | 0.998 | 0.807 |
| DcomA2 | | | | | | 1.026 | 0.74 |
| DcomB10 | T | A H | P | N W Y | Q | 0.87 | 0.735 |
| DcomC8 | S | A A | P | N W Y | Q | 0.978 | 0.763 |
| DcomD7 | T | A Y | P | N W Y | Q | 1.083 | 0.794 |
| DhuG5 | | | | | | | |
| DhuH8 | | | | | | | |
| DcomD11 | A | A A | P | N W H | Q | 1.125 | 0.752 |
| DcomE11 | A | A H | P | N W H | Q | 0.973 | 0.732 |

Primers for combinatorial mutation

dH5762 TCTCTGGAGATGGTGAATTTACGTACTGCTATCTGGATT
dL27def CTAAGTAGTTCTTTTGGTTGTTATAACAGACTCTGGCTGGA
H1-35 TGGAGCCTGGCGGACCCAGGHCATCCAATATCTACTAAAGGTGAATCCAGA
H2-5762a TCTCTGGAGATGGTGAATCTATCCTTTAGGGMTGGCGTATAGTTGGCCGTACTGCTATCTGGATT
H2-5762b TCTCTGGAGATGGTGAATCTATCCTTTAGGTRTGGCGTATAGTTGGCCGTACTGCTATCTGGATT
L1-27def1 CTAAGTAGTTCTTTTGGTTGTRGTRGYTTAACAGACTCTGGCTGGA
L1-27def2 CTAAGTAGTTCTTTTGGTTGCSGTRGYTTAACAGACTCTGGCTGGA
L1-27def3 CTAAGTAGTTCTTTTGGTTGTRGCKGYTTAACAGACTCTGGCTGGA
L1-27def4 CTAAGTAGTTCTTTTGGTTGCSGCKGYTTAACAGACTCTGGCTGGA
L1-27def5 CTAAGTAGTTCTTTTGGTTGTRCCAGYTTAACAGACTCTGGCTGGA
L1-27def6 CTAAGTAGTTCTTTTGGTTGCSCCAGYTTAACAGACTCTGGCTGGA

FIGURE 6

Beneficial mutations chosen for combinatorial library

| CDRs | H1 | H2 | H3 | L1 | L3 | Screen | Screen |
|--------------|---------------|-------------|------|--------------|-------|--------|--------|
| Kabat Number | 32 35b | 59 | 100e | 27d 28 33 | 91 94 | kon | koff |
| wild type | S G | Y | M | H N L | G V | | |
| HuI-77 | S G | Y | M | H N L | V | | |
| Mutations | P W L A | S A P | Q | L Y F S W | S | | |

Beneficial combinatorial mutants

| | | | | | | | |
|----------|-----|---|---|-------|-----|-------|-------|
| Qh2b-B7 | S G | A | Q | H N L | S | | |
| QH2b-A3 | S G | S | Q | H N L | | | |
| Qcom1B6 | P W | S | Q | S W L | S | 1.319 | 0.534 |
| Qcom1B8 | P W | S | Q | S Y L | S | 1.266 | 0.497 |
| Qcom1E7 | | | | | | 1.247 | 0.46 |
| Qcom1G10 | | | | | | 1.282 | 0.452 |
| Qcom2G2 | | | | | | 1.304 | 0.402 |
| Qcom1C3 | P W | A | Q | S W L | S | 1.342 | 0.535 |
| Qcom2A2 | | | | | | 1.605 | 0.647 |
| Qcom1G3 | | | | | | 1.274 | 0.464 |
| Qcom1D3 | P W | T | Q | S W L | S | 1.647 | 0.984 |
| QhuD9 | | | | | | | |
| QhuD93 | | | | | | | |
| Qcom1E3 | P W | A | Q | S Q L | S | 1.225 | 0.347 |
| Qcom2F6 | | | | | | 1.311 | 0.321 |
| Qcom1H6 | P W | S | Q | S Q L | S | 1.295 | 0.323 |
| Qcom1H7 | P W | A | Q | H Q F | S F | 1.634 | 1.08 |
| Qcom2A4 | P A | A | Q | S Y L | S | 1.304 | 0.265 |
| Qcom2B11 | P W | A | Q | H Y L | S | 1.11 | 0.221 |
| Qcom2C1 | P W | Y | Q | S W F | S | 1.189 | 0.213 |
| Qcom2D9 | P W | S | Q | H W L | S | 1.101 | 0.209 |
| Qcom2E3 | P W | A | Q | H W L | S | 1.117 | 0.248 |

Primers for combinatorial mutation

dL27d-33 CTT CTG CAG GTA CCA TTC GTTA TAC AAT GCT CTG ACT AGA
H1-35b1 TGG GGG CTG ACG GAT CCA CMA CAC ACC CAT TCC AGR AGT GCT GAG TGA GAA CCC AGA
H1-35b2 TGG GGG CTG ACG GAT CCA GSC CAC ACC CAT TCC AGR AGT GCT GAG TGA GAA CCC AGA
H2-59 GCT CTT CAG AGA TGG GTT AGV GTA TTT ATT GTC ATC CCA C
L27d1 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC CCA ACT CRA TAC AAT GCT CTG ACT AGA
L27d2 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC GTA ACT CRA TAC AAT GCT CTG ACT AGA
L27d3 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC CTG ACT CRA TAC AAT GCT CTG ACT AGA
L27d4 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC CCA ACT GTG TAC AAT GCT CTG ACT AGA
L27d5 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC GTA ACT GTG TAC AAT GCT CTG ACT AGA
L27d6 CTT CTG CAG GTA CCA TTC MAA ATA GGT GTT TCC CTG ACT GTG TAC AAT GCT CTG ACT AGA

FIGURE 7

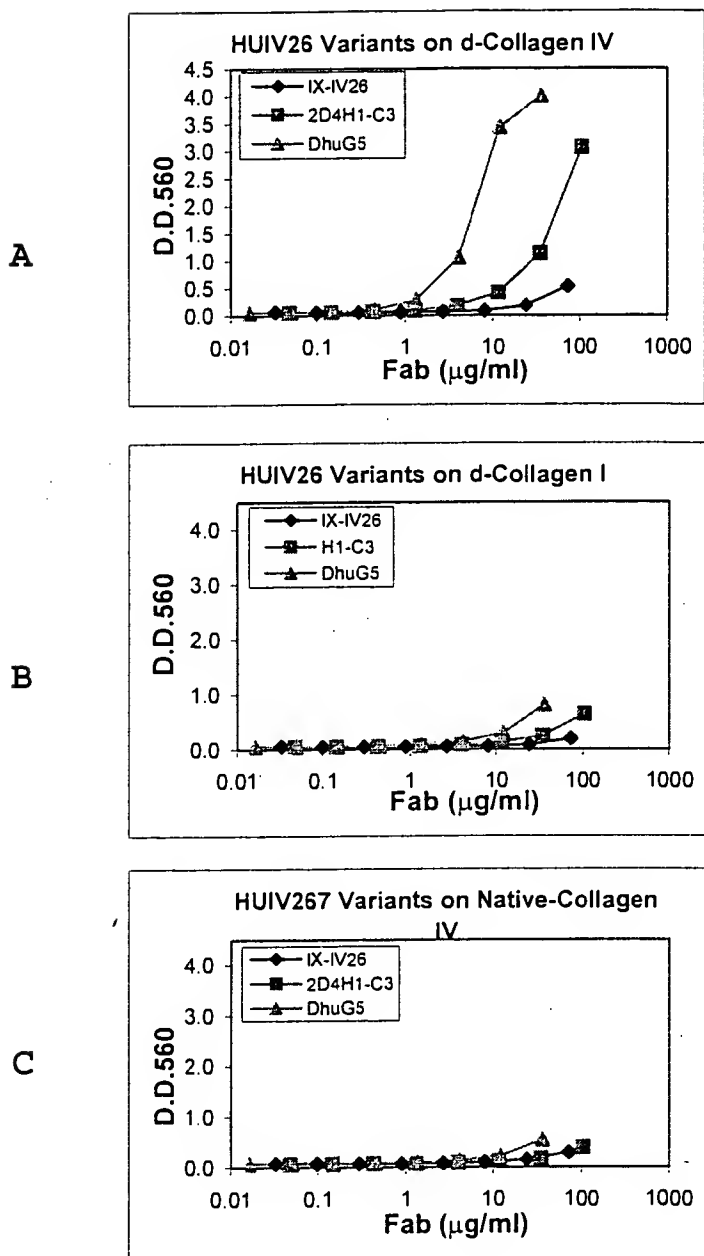
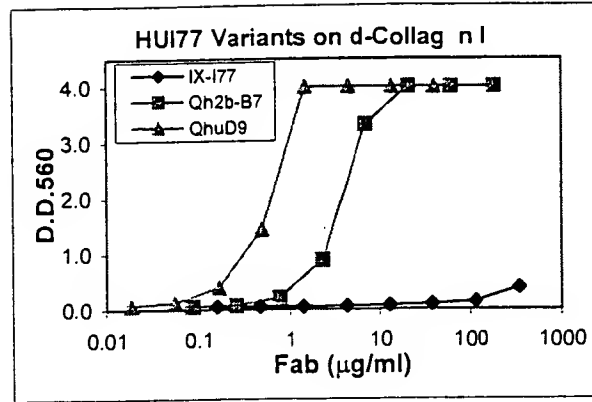
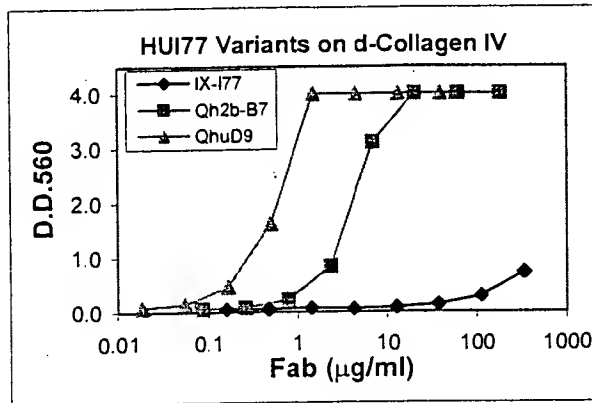


FIGURE 8

A



B



C

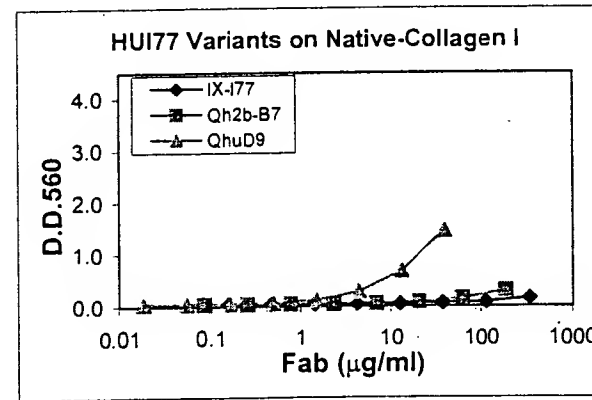


FIGURE 9

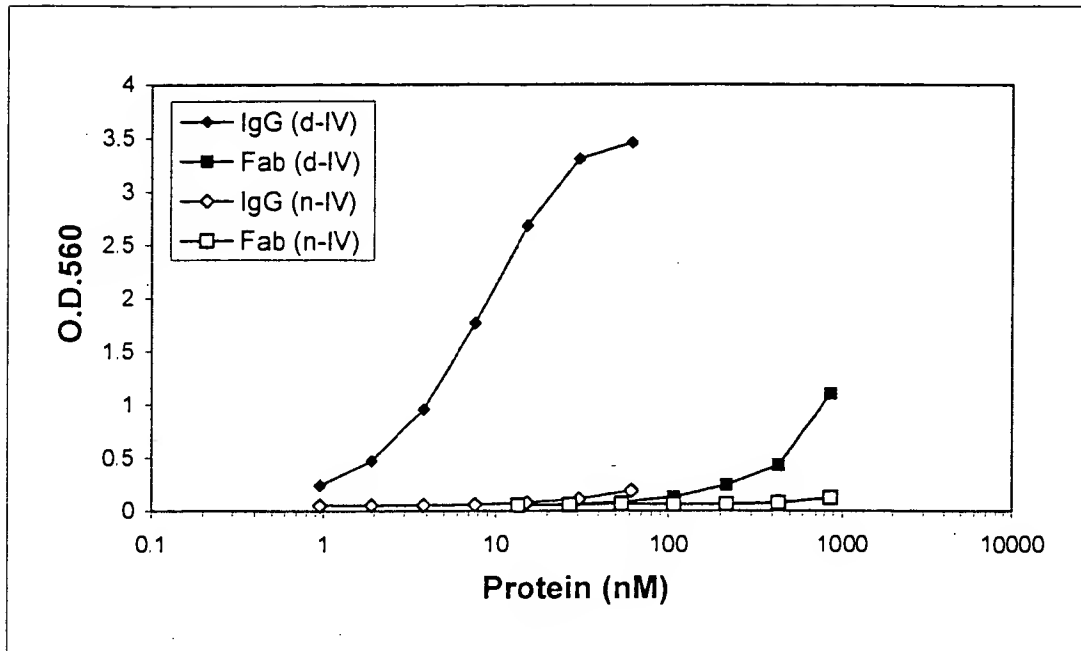


FIGURE 10

Cell Proliferation (Cell Number)

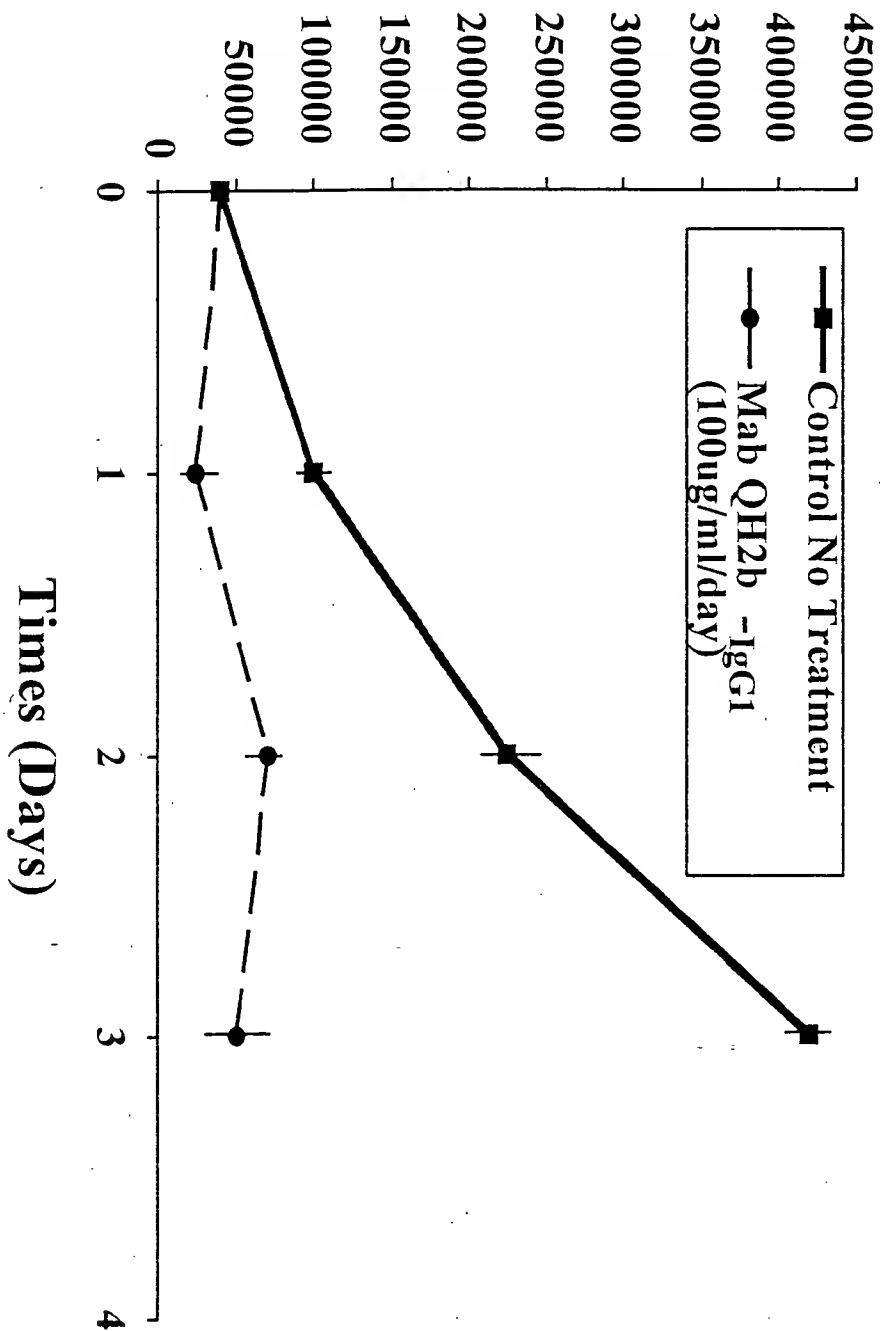


FIGURE 11